

Claims:

1. A reduced seed-oil content plant cell that expresses a seed-oil suppressing gene under control of a plant-active promoter, wherein said plant exhibits a reduction in seed-oil and a concomitant increase in plant carbohydrate, protein or both and wherein said seed-oil suppressing gene is selected from the group consisting of a mutant allele of a gene naturally occurring in said plant and a transgene.
2. A reduced seed-oil content plant cell of claim 1, which is selected from the group consisting of cotton, corn, soybean, canola and wheat.
3. A reduced seed-oil content plant cell of claim 2, which is a cotton plant cell.
4. A reduced seed-oil content plant which comprises a cell of claim 1.
5. A reduced seed-oil content plant of claim 4, wherein said cotton plant has enhanced fiber yield.
6. A reduced seed-oil content plant of claim 1, wherein said seed-oil suppressing gene is a mutant allele of a gene naturally occurring in said plant.
7. A reduced seed-oil content plant of claim 4, which is an elite cultivar.
8. A reduced seed-oil content plant of claim 4, which is a primitive cultivar.
9. A reduced seed-oil content plant of claim 4, wherein said seed-oil suppressing gene is introduced into the germplasm of said elite cultivar.
10. A reduced seed-oil content plant of claim 4, wherein said seed-oil suppressing gene controls seed-oil content by suppressing seed-oil biosynthesis.

11. A reduced seed-oil content plant of claim 4, wherein said seed-oil suppressing gene controls seed-oil content by suppressing seed-oil storage.
12. A reduced seed-oil content plant of claim 4, wherein said seed-oil suppressing gene is generated within the germplasm of said plant by random mutagenesis.
13. A reduced seed-oil content plant of claim 12, wherein said seed-oil suppressing gene is mutagenized by exposure to ethyl methanesulfonate.
14. A reduced seed-oil content plant of claim 4, wherein said seed-oil suppressing gene is identified and isolated from a mutagenized seed stock.
15. A reduced seed-oil content plant of claim 4, wherein expression of said seed-oil suppressing gene suppresses at least one biosynthetic step in oil biosynthesis.
16. A reduced seed-oil content plant of claim 4, wherein expression of said seed-oil suppressing gene suppresses a gene selected from the group consisting of carbonic anhydrase, ACCase, lysophosphatidic acid acyltransferase (LPAT), diacylglycerol acyltransferase (DGAT), oleosin and any combination thereof.
17. A reduced seed-oil content plant of claim 15, wherein said seed-oil suppressing gene suppresses a gene early in the oil biosynthetic pathway and a gene late in the oil biosynthetic pathway.
18. A reduced seed-oil content plant of claim 17, wherein said gene that is early in the seed-oil biosynthesis pathway is selected from the group consisting of the CA gene and the ACCase gene, and wherein said gene that is late in the seed-oil biosynthesis pathway is selected from the group consisting of the LPAT gene and the DGAT gene.
19. A reduced seed-oil content plant of claim 4, wherein said seed-oil suppressing gene is a transgene.

20. A reduced seed-oil content plant of claim 19, wherein expression of said transgene suppresses seed-oil biosynthesis.

21. A reduced seed-oil content plant of claim 19, wherein expression of said transgene suppresses at least one biosynthetic step in oil biosynthesis.

22. A reduced seed-oil content plant of claim 21, wherein expression of said transgene suppresses a gene selected from the group consisting of carbonic anhydrase, ACCase, lysophosphatidic acid acyltransferase, diacylglycerol acyltransferase, oleosin and any combination thereof.

23. A reduced seed-oil content plant of claim 21, wherein said transgene suppresses a gene early in the oil biosynthetic pathway and a gene late in the oil biosynthetic pathway.

24. A reduced seed-oil content plant of claim 21, wherein said seed-oil suppressing transgene is a nucleic acid that encodes an RNAi sequence for a gene that is early in the seed-oil biosynthesis pathway and for a gene that is late in the seed-oil biosynthesis pathway.

25. A reduced seed-oil content plant of claim 24, wherein said gene that is early in the seed-oil biosynthesis pathway is selected from the group consisting of the CA gene and the ACCase gene, and wherein said gene that is late in the seed-oil biosynthesis pathway is selected from the group consisting of the LPAT gene and the DGAT gene.

26. A reduced seed-oil content plant of claim 4, wherein said seed-oil suppressing gene is selected from the group consisting of a cosuppression directing nucleic acid, an antisense nucleic acid, a nucleic acid that encodes an immunomodulation protein, a nucleic acid that encodes a ribozyme, a nucleic acid that encodes a transcription factor suppressor and a nucleic acid that encodes an RNAi sequence.

27. A reduced seed-oil content plant of claim 19, wherein said transgene is operatively linked to a constitutive promoter.

28. A reduced seed-oil content plant of claim 27, wherein said constitutive promoter is selected from the group consisting of the 35S promoter from cauliflower mosaic virus, the maize ubiquitin promoter, the peanut chlorotic streak caulimovirus promoter, a Chlorella virus methyltransferase gene promoter, the full-length transcript promoter from figwort mosaic virus, the rice actin promoter, pEMU promoter, MAS promoter, the maize H3 histone promoter and an Agrobacterium gene promoter.

29. A reduced seed-oil content plant of claim 19, wherein said transgene is operatively linked to a seed-specific promoter.

30. A reduced seed-oil content plant of claim 29, wherein said seed-specific promoter is selected from the group consisting of the cotton alpha-globulin promoter, the napin gene promoter, the soybean alpha-conglycinin gene promoter, the soybean beta-conglycinin gene promoter and the soybean lectin promoter.

31. A reduced seed-oil content plant of claim 29, wherein said seed-specific promoter is generated by operable linkage of a genetic element that directs seed-specific expression to a core promoter sequence.

32. A reduced seed-oil content plant of claim 19, wherein said promoter is activated by application of an external stimulus.

33. A reduced seed-oil content plant of claim 32, wherein said seed-oil suppressing gene is expressed in the presence of said external stimulus.

34. A reduced seed-oil content plant of claim 32, wherein said external stimulus is copper, a benzenesulfonamide herbicide safener, a glucocorticosteroid hormone, estradiol and ecdysterodial activity.

35. A reduced seed-oil content plant of claim 32, wherein expression of said seed-oil suppressing gene, after activation, continues to be expressed in the absence of said external stimulus.

36. A reduced seed-oil content plant of claim 19, wherein said seed-oil suppressing gene is operably linked to a promoter selected from the group consisting of an inducible promoter and a repressible promoter.

37. A reduced seed-oil content plant of claim 36, wherein said inducible promoter is selected from the group consisting of the promoter from the ACE1 system, the promoter of the maize Intron 2 gene, the promoter of the Tet repressor from Tn10, the phosphate-deficiency responsive promoter from a phosphate-starvation responsive beta-glucosidase gene from *Arabidopsis*, the synthetic promoter containing a 235bp sulfur deficiency response element from a soybean beta-conglycinin gene linked to a 35S core promoter sequence, the inducible promoter from a steroid hormone gene the transcriptional activity of which is induced by a glucocorticosteroid hormone and XVE.

38. A reduced seed-oil content plant of claim 36, wherein said promoter is a seed-specific promoter.

39. A reduced seed-oil content plant of claim 38, wherein said promoter is the cotton alpha-globulin promoter (AGP).

40. A reduced seed-oil content plant of claim 35, wherein said plant comprises an excisable blocking sequence that prevents expression of said seed-oil suppressing gene.

41. A reduced seed-oil content plant of claim 35, wherein the seed-oil content of said plant is reduced to a level of 1% to 17% of the fuzzy whole seed weight.

42. A reduced seed-oil content plant of claim 35, wherein stable pools of sucrose are generated in said plant that are available to increase, in a sustained fashion, the production of commercially valuable cellulosic, starch or protein macromolecules.

43. A reduced seed-oil content plant of claim 19, wherein said seed-oil suppressing transgene is a nucleic acid that encodes an RNAi sequence for a gene that is early in the seed-oil biosynthesis pathway and for a gene that is late in the seed-oil biosynthesis pathway.

44. A reduced seed-oil content plant of claim 43, wherein said gene that is early in the seed-oil biosynthesis pathway is selected from the group consisting of the CA gene and the ACCase gene, and wherein said gene that is late in the seed-oil biosynthesis pathway is selected from the group consisting of the LPAT gene and the DGAT gene.

45. A method for making a reduced seed-oil content plant of claim 4, which comprises:

(a) transfecting a plant cell with a transgene that suppresses a gene selected from the group consisting of carbonic anhydrase, ACCase, lysophosphatidic acid acyltransferase, diacylglycerol acyltransferase, oleosin and any combination thereof under control of a plant-active promoter; and

(b) regenerating a whole plant from said plant cell.

46. A method of claim 45, wherein said transgene suppresses a gene early in the oil biosynthetic pathway and a gene late in the oil biosynthetic pathway.

47. A method of claim 46, wherein said gene that is early in the seed-oil biosynthesis pathway is selected from the group consisting of the CA gene and the ACCase gene, and wherein said gene that is late in the seed-oil biosynthesis pathway is selected from the group consisting of the LPAT gene and the DGAT gene.

48. A method of claim 45, wherein said seed-oil suppressing transgene is a nucleic acid that encodes an RNAi sequence for a gene that is early in the seed-oil biosynthesis pathway and for a gene that is late in the seed-oil biosynthesis pathway.

49. A method of claim 45, wherein said seed-oil suppressing gene is selected from the group consisting of a cosuppression directing nucleic acid, an antisense nucleic acid, a nucleic acid that encodes an immunomodulation protein, a nucleic acid that encodes a

ribozyme, a nucleic acid that encodes a transcription factor suppressor and a nucleic acid that encodes an RNAi sequence.

50. A method of claim 45, wherein said promoter is a constitutive promoter.

51. A method of claim 50, wherein said constitutive promoter is selected from the group consisting of the 35S promoter from cauliflower mosaic virus, the maize ubiquitin promoter, the peanut chlorotic streak caulimovirus promoter, a *Chlorella* virus methyltransferase gene promoter, the full-length transcript promoter from figwort mosaic virus, the rice actin promoter, pEMU promoter, MAS promoter, the maize H3 histone promoter and an *Agrobacterium* gene promoter.

52. A method of claim 45, wherein said promoter is a seed-specific promoter.

53. A method of claim 52, wherein said seed-specific promoter is selected from the group consisting of the cotton alpha-globulin promoter, the napin gene promoter, the soybean alpha-conglycinin gene promoter, the soybean beta-conglycinin gene promoter and the soybean lectin promoter.

54. A method of claim 52, wherein said seed-specific promoter is generated by operable linkage of a genetic element that directs seed-specific expression to a core promoter sequence.

55. A method of claim 52, wherein said promoter is activated by application of an external stimulus.

56. A method of claim 55, wherein said seed-oil suppressing gene is expressed in the presence of said external stimulus.

57. A method of claim 55, wherein said external stimulus is copper, a benzenesulfonamide herbicide safener, a glucocorticosteroid hormone, estradiol and ecdysteroidal activity.

58. A method of claim 55, wherein expression of said seed-oil suppressing gene, after activation, continues to be expressed in the absence of said external stimulus.

59. A method of claim 55, wherein said promoter is selected from the group consisting of an inducible promoter and a repressible promoter.

60. A method of claim 57, wherein said inducible promoter is selected from the group consisting of the promoter from the ACE1 system, the promoter of the maize Intron 2 gene, the promoter of the Tet repressor from Tn10, the phosphate-deficiency responsive promoter from a phosphate-starvation responsive beta-glucosidase gene from *Arabidopsis*, the synthetic promoter containing a 235bp sulfur deficiency response element from a soybean beta-conglycinin gene linked to a 35S core promoter sequence, the inducible promoter from a steroid hormone gene the transcriptional activity of which is induced by a glucocorticosteroid hormone and XVE.

61. A method of claim 59, wherein said promoter is a seed-specific promoter.

62. A method of claim 61, wherein said promoter is the cotton alpha-globulin promoter (AGP).

63. A method of claim 45, wherein the seed-oil content of said plant is reduced to a level of 1% to 17% of the fuzzy whole seed weight.

64. A method of claim 45, wherein stable pools of sucrose are generated in said plant that are available to increase, in a sustained fashion, the production of commercially valuable cellulosic, starch or protein macromolecules.

65. A breeding method for producing an enhanced yield self-pollinating plant that contains a yield enhancing gene, which comprises:

- (a) providing an elite recurrent parent plant;
- (b) providing a donor parent plant that contains said yield enhancing gene and that contains at least one phenotypic trait;

(c) crossing said elite recurrent parent plant with said donor parent plant to produce an F1 progeny plant;

(d) crossing said F1 progeny plant with said elite recurrent parent plant to produce a BC1F1 progeny plant that contains said yield enhancing gene;

(e) self-pollinating said BC1F1 progeny plant to produce a BC1F2 progeny plant that contains said yield enhancing gene;

(f) self-pollinating said BC1F2 progeny plant to produce BC1F2:3 plants that contain said yield enhancing gene;

(g) self-pollinating said BC1F2:3 plants;

(h) screening said BC1F2:3 plants for zygosity of said yield enhancing gene;

(i) collecting seed of said BC1F2:3 plants that are homozygous for said yield enhancing gene, which is BC1F2:4 seed; and

(j) germinating said seed to produce an enhanced yield self-pollinating plant that contains said yield enhancing gene.

66. A breeding method for producing an enhanced yield self-pollinating plant that contains a yield enhancing gene, which comprises:

(a) providing an elite recurrent parent plant;

(b) providing a donor parent plant that contains said yield enhancing gene and that contains at least one phenotypic trait;

(c) crossing said elite recurrent parent plant with said donor parent plant to produce an F1 progeny plant;

(d) crossing said F1 progeny plant with said elite recurrent parent plant to produce a BC1F1 progeny plant that contains said yield enhancing gene;

(e) self-pollinating said BC1F1 progeny plant to produce a BC1F2 progeny plant that contains said yield enhancing gene;

(f) self-pollinating said BC1F2 progeny plant one or more additional times to produce a BC1F3, BC1F4, BC1F5, BC1F6 or later generation of progeny plants that contain said yield enhancing gene;

(g) self-pollinating said progeny plants of step (f);

(h) screening said progeny plants of step (f) for zygosity of said yield enhancing gene;

(i) collecting the seed of said progeny plants that are homozygous for said yield enhancing gene; and

(j) germinating said seed to produce an enhanced yield self-pollinating plant that contains said yield enhancing gene.

67. A breeding method of claim 65 or 66, wherein said screening for zygoty is performed by planting a progeny row and determining the extent to which plants in said progeny row exhibit a phenotypic trait characteristic of said yield enhancing gene.

68. A breeding method of claim 65 or 66, wherein said screening for zygoty is performed by testing for the expression of said yield enhancing gene.

69. A breeding method of claim 65 or 66, wherein said screening for zygoty is performed by testing for the presence of the gene in tissues of said progeny plants by PCR.

70. A breeding method for producing an enhanced yield self-pollinating plant that contains a yield enhancing gene, which comprises:

(a) providing an elite recurrent parent plant;

(b) providing a donor parent plant that contains said yield enhancing gene and that contains at least one phenotypic trait;

(c) crossing said elite recurrent parent plant with said donor parent plant to produce an F1 progeny plant;

(d) crossing said F1 progeny plant with said elite recurrent parent plant to produce a BC1F1 progeny plant that contains said yield enhancing gene;

(e) self-pollinating said BC1F1 progeny plant to produce a BC1F2 progeny plant that contains said yield enhancing gene;

(f) self-pollinating said BC1F2 progeny plant to produce BC1F2:3 plants that contain said yield enhancing gene;

(g) self-pollinating said BC1F2:3 plants;

(h) screening said BC1F2:3 plants for zygoty of said yield enhancing gene;

- (i) collecting seed of said BC1F2:3 plants that contain said yield enhancing gene, which is BC1F3:4 seed;
- (j) germinating said BC1F3:4 seed to produce BC1F3:4 plants;
- (k) self-pollinating said BC1F3:4 plants;
- (l) screening said BC1F3:4 plants for zygosity of said yield enhancing gene;
- (m) collecting seed of said BC1F3:4 plants that are homozygous for said yield enhancing gene, which is BC1F3:5 seed; and
- (n) germinating said seed to produce an enhanced yield self-pollinating plant that contains said yield enhancing gene.

71. A breeding method for producing an enhanced yield self-pollinating plant that contains a yield enhancing gene, which comprises:

- (a) providing an elite recurrent parent plant;
- (b) providing a donor parent plant that contains said yield enhancing gene and that contains at least one phenotypic trait;
- (c) crossing said elite recurrent parent plant with said donor parent plant to produce an F1 progeny plant;
- (d) crossing said F1 progeny plant with said elite recurrent parent plant to produce a BC1F1 progeny plant that contains said yield enhancing gene;
- (e) self-pollinating said BC1F1 progeny plant to produce a BC1F2 progeny plant that contains said yield enhancing gene;
- (f) self-pollinating said BC1F2 progeny plant one or more additional times to produce a BC1F3, BC1F4, BC1F5, BC1F6 or later generation of progeny plants that contain said yield enhancing gene;
- (g) self-pollinating said progeny plants of step (f);
- (h) screening said progeny plants of step (f) for zygosity of said yield enhancing gene;
- (i) collecting seed of said progeny plants of step (f) that contain said yield enhancing gene;
- (j) germinating said seed of step (i) to produce plants;
- (k) self-pollinating said plants of step (j);
- (l) screening said plants of step (j) for zygosity of said yield enhancing gene;

(m) collecting seed of said plants of step (j) that are homozygous for said yield enhancing gene; and

(n) germinating said seed to produce an enhanced yield self-pollinating plant that contains said yield-enhancing gene.

72. A breeding method of claim 70 or 71, wherein said screening for zygoty is performed by planting a progeny row and determining the extent to which plants in said progeny row exhibit a phenotypic trait characteristic of said yield enhancing gene.

73. A breeding method of claim 70 or 71, wherein said screening for zygoty is performed by testing for the expression of said yield enhancing gene.

74. A breeding method of claim 70 or 71, wherein said screening for zygoty is performed by testing for the presence of the gene in tissues of said progeny plants by PCR.

75. A breeding method for producing an enhanced yield self-pollinating plant that contains a yield enhancing gene, which comprises:

- (a) providing an elite recurrent parent plant;
- (b) providing a donor parent plant that contains said yield enhancing gene and that contains at least one phenotypic trait;
- (c) crossing said elite recurrent parent plant with said donor parent plant to produce an F1 progeny plant;
- (d) crossing said F1 progeny plant with said elite recurrent parent plant to produce a BC1F1 progeny plant that contains said yield enhancing gene;
- (e) self-pollinating said BC1F1 progeny plant to produce a BC1F2 progeny plant that contains said yield enhancing gene;
- (f) self-pollinating said BC1F2 progeny plant to produce BC1F2:3 plants that contain said yield enhancing gene;
- (g) self-pollinating said BC1F2:3 plants;
- (h) screening said BC1F2:3 plants for zygoty of said yield enhancing gene;
- (i) collecting seed of said BC1F2:3 plants that contain said yield enhancing gene, which is BC1F3:4 seed;

- (j) germinating said BC1F3:4 seed to produce BC1F3:4 plants;
- (k) self-pollinating said BC1F3:4 plants;
- (l) screening said BC1F3:4 plants for zygoty of said yield enhancing gene;
- (m) collecting seed of said BC1F3:4 plants that contain said yield enhancing gene, which is BC1F4:5 seed;
- (n) germinating said BC1F4:5 seed to produce BC1F4:5 plants;
- (o) self-pollinating said BC1F4:5 plants;
- (p) screening said BC1F4:5 plants for zygoty of said yield enhancing gene;
- (q) collecting seed of said BC1F4:5 plants that are homozygous for said yield enhancing gene, which is BC1F4:6 seed; and
- (r) germinating said seed to produce an enhanced yield self-pollinating plant that contains said yield enhancing gene.

76. A breeding method for producing an enhanced yield self-pollinating plant that contains a yield enhancing gene, which comprises:

- (a) providing an elite recurrent parent plant;
- (b) providing a donor parent plant that contains said yield enhancing gene and that contains at least one phenotypic trait;
- (c) crossing said elite recurrent parent plant with said donor parent plant to produce an F1 progeny plant;
- (d) crossing said F1 progeny plant with said elite recurrent parent plant to produce a BC1F1 progeny plant that contains said yield enhancing gene;
- (e) self-pollinating said BC1F1 progeny plant to produce a BC1F2 progeny plant that contains said yield enhancing gene;
- (f) self-pollinating said BC1F2 progeny plant one or more additional times to produce a BC1F3, BC1F4, BC1F5, BC1F6 or later generation of progeny plants that contain said yield enhancing gene;
- (g) self-pollinating said progeny plants of step (f);
- (h) screening said progeny plants of step (f) for zygoty of said yield enhancing gene;
- (i) collecting seed of said progeny plants of step (f) that contain said yield enhancing gene;
- (j) germinating said seed to produce plants;

(k) self-pollinating said plants of step (j);
(l) screening said plants of step (j) for zygoty of said yield enhancing gene;
(m) collecting seed of said plants of step (j) that contain said yield enhancing gene;
(n) germinating said seed of step (m) to produce plants;
(o) self-pollinating said plants of step (n);
(p) screening said plants of step (n) for zygoty of said yield enhancing gene;
(q) collecting seed of said plants of step (n) that are homozygous for said yield enhancing gene;
(r) germinating said seed of step (q) to produce an enhanced yield self-pollinating plant that contains said yield enhancing gene.

77. A breeding method of claim 75 or 76, wherein said screening for zygoty is performed by planting a progeny row and determining the extent to which plants in said progeny row exhibit a phenotypic trait characteristic of said yield enhancing gene.

78. A breeding method of claim 75 or 76, , wherein said screening for zygoty is performed by testing for the expression of said yield enhancing gene.

79. A breeding method of claim 75 or 76, wherein said screening for zygoty is performed by testing for the presence of the gene in tissues of said progeny plants by PCR.

80. A method of claim 75 which further comprises repeating steps (k) - (r) for generations of heterozygous progeny plants subsequent to BC1F4:5.

81. A method of any of claims 65, 66, 70, 71, 75 or 76 wherein said yield enhancing trait is selected from the group consisting of seed-oil suppression, delayed leaf senescence, enhanced leaf photosynthesis, enhanced leaf production of sucrose, enhance leaf export of sucrose, enhanced translocation of sucrose in the plant vasculature, reduced plant respiratory losses, reduced plant photorespiratory losses, reduced carbohydrate use in non-fruit plant tissue, enhanced movement of sucrose into the desired plant organ or tissue, and any combination thereof.

82. A method of any of claims 65, 66, 70, 71, 75 or 76 wherein said phenotypic trait is selected from the group consisting of dwarfing, short stature, more determinate growth habit, precocious flowering, intense flowering, rapid fruit development, medium to large seeds, large bolls, high fruit retention, high lint percent, low micronaire, cluster fruiting, insect protection, and any combination thereof.

83. A method of any of claims 65, 66, 70, 71, 75 or 76 wherein said elite recurrent parent plant is selected for a quality selected from the group consisting of yield, adaptation, fiber quality, agronomic performance and transgenic traits.

84. A method of any of claims 65, 66, 70, 71, 75 or 76 wherein said yield enhancing gene is selected from the group consisting of a mutant allele of a gene naturally occurring in said plant and a transgene.

85. A method of any of claims 65, 66, 70, 71, 75 or 76 wherein said donor parent plant is produced by directly transforming a recurrent plant containing said at least one phenotypic trait with said yield enhancing gene.

86. A method of any of claims 65, 66, 70, 71, 75 or 76 wherein said donor parent plant is produced by crossing a yield enhancing gene donor plant with a recurrent plant containing said at least one phenotypic trait and selecting progeny plants that contain both said yield enhancing gene and said at least one phenotypic trait.

87. A method of any of claims 65, 66, 70, 71, 75 or 76 wherein said donor parent plant is produced by crossing and backcrossing a yield enhancing gene donor plant with a recurrent plant containing said at least one phenotypic trait and selecting progeny plants that contain both said yield enhancing gene and said at least one phenotypic trait.